

subsequences under conditions that generate one or more second signals arising from said selected targeted nucleic acid, at least one of whose subsequences has been extended, in said sample, wherein said second signal comprises a representation of (i) the length between occurrences of target subsequences, at least one of which has been extended, in said nucleic acid, and (ii) the identities of said selected target subsequences, at least one of which has been extended, in said selected targeted nucleic acid or identities of said target subsequences, at least one of which has been extended, among which are included the target subsequences in said selected targeted nucleic acid; and

(e). searching a nucleotide sequence database to determine sequences that match or the absence of any sequences that match one or more of said selected targeted nucleic acids having at least one extended subsequence and represented by said generated second signals, said database comprising a plurality of known nucleotide sequences of nucleic acids that may be present in the sample, wherein a sequence from said database is determined to match said selected targeted nucleic acid providing a generated second signal when the sequence from said database has both (i) the same length between occurrences of target subsequences, at least one of which has been extended, as is represented by the generated signal, and (ii) the same target subsequences, at least one of which has been extended, as are represented by the generated signal, or target subsequences, at least one of which has been extended, that are members of the same sets of target subsequences represented by the generated signal,

whereby a matched nucleic acid in said sample is identified, classified, or quantified.

7. (Amended) The method of claim 1 wherein said method additionally includes recovering a fragment of a nucleic acid in the sample which generates said signal after steps (b) or (d);
- sequencing said fragment to determine at least a partial sequence for said fragment; and verifying that said sample comprises a nucleic acid having a sequence comprising at least a portion of said determined sequence.

11. (Amended) A method for extending the sequence in a length-subsequence combination of one or more nucleic acids in a sample comprising a plurality of nucleic acids having different nucleotide sequences without sequencing, said method comprising:

(a) probing said sample with one or more recognition means wherein each recognition means recognizes a different target nucleotide subsequence or a different set of target nucleotide subsequences to provide one or more targeted nucleic acids;

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(b) generating one or more first signals from said sample probed by said recognition means, each generated first signal arising from a targeted nucleic acid in said sample and comprising a representation of (i) the length between occurrences of target subsequences in said targeted nucleic acid, and (ii) the identities of said target subsequences in said targeted nucleic acid or identities of said target subsequences among which are included the target subsequences in said targeted nucleic acid;

(c) selecting one or more targeted nucleic acids based on their corresponding first signals; and

(d) extending sequence information from one or more target subsequences in said targeted nucleic acid by one or more nucleotides providing one or more extended subsequences under conditions that generate one or more second signals arising from selected targeted nucleic acid in said sample at least one of whose subsequences has been extended, wherein said second signal comprises a representation of (i) the length between occurrences of target subsequences, at least one of which has been extended, in said nucleic acid, and (ii) the identities of said target subsequences, at least one of which has been extended, in said selected targeted nucleic acid or identities of said target subsequences, at least one of which has been extended, among which are included the target subsequences in said selected targeted nucleic acid;

whereby a matched nucleic acid in said sample has an extended sequence in said length-subsequence combination.

In the Drawings

In Figure 3, replace the title with the following title:

B4 "FIG. 3. Oligo-competition set up. Oligo-competition primers are set up on the J or R side based on the predicted sequence of the GeneCalled™ fragment. Oligo-competition reactions involve J23 and R23 primers with a fifty fold excess of the oligo-competition primers."

In Figure 6, replace the title with the following title:

B5 "FIG. 6. Example of identification of the first base on the 3' side of the restriction enzyme sites on the R and J side for each QEA peak in the BspHI and BglII double digest of rat liver cDNA. (see text for details)"